

L5 ANSWER 1 OF 1

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LOCUS (LOC): BF509252 GenBank (R)
GenBank ACC. NO. (GBN): **BF509252**
CAS REGISTRY NO. (RN): 307875-04-3
SEQUENCE LENGTH (SQL): 791
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 6 Dec 2000
DEFINITION (DEF): UI-H-BI4-aow-c-07-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens
cDNA clone IMAGE:3086220 3', mRNA sequence.
KEYWORDS (ST): EST
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates;
Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 270 a 151 c 144 g 226 t
COMMENT:
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bona fide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLY(A)=Yes.
REFERENCE:
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..791	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:3086220" /clone-lib="NCI-CGAP-Sub8" /lab-host="DH10B (Life Technologies)" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; NCI-CGAP-Sub8 is a subtracted library derived from NCI-CGAP-Sub5. The NCI-CGAP-Sub8 library had 2.5 million recombinants. A single-stranded DNA preparation of NCI-CGAP-Sub5 was used as a tracer in a subtractive hybridization with a driver comprising: a pool of clones from NCI-CGAP-Sub5 (IMAGE

clone Ids 2732833-2737415, 3068040-3069191; 25% of the driver population), a pool of clones from NCI-CGAP-Sub4 (IMAGE clone Ids 2723592-2729326; 25% of the driver population), NCI-CGAP-Sub6 (pool AIF-AJU, IMAGE Ids 2728969-2733190; 25% of the driver population), and NCI-CGAP-Sub7 (IMAGE Ids 3069192-3072238, 3081864-3084550 ; 25% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. *Genome Research* 6, 791-806. TAG-LIB=NCI-CGAP-Lu5 TAG-TISSUE=lung TAG-SEQ=CAAC"

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L3 ANSWER 1 OF 1

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LOCUS (LOC): HSU95825 **GenBank (R)**
GenBank ACC. NO. (GBN): **U95825**
CAS REGISTRY NO. (RN): 225494-81-5
SEQUENCE LENGTH (SQL): 5253
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 5 Apr 1999
DEFINITION (DEF): Human androgen-induced prostate proliferative shutoff associated protein (AS3) mRNA, complete cds.
SOURCE:
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates;
Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 1755 a 944 c 1074 g 1480 t
COMMENT:
On Apr 5, 1999 this sequence version replaced gi:4539617.
REFERENCE:
AUTHOR (AU): Geck, P.; Szelei, J.; Jimenez, J.; Soto, A.M.; Sonnenschein, C.
TITLE (TI): Androgen-induced proliferative shutoff in prostate cancer cells
JOURNAL (SO): Proc. Annu. Meet. Am. Assoc. Cancer Res., 37, 223-223 (1996)
REFERENCE:
AUTHOR (AU): Geck, P.; Szelei, J.; Jimenez, J.; Sonnenschein, C.; Soto, A.M.
TITLE (TI): Early gene expression during androgen-induced inhibition of proliferation of prostate cancer cells:
a
JOURNAL (SO): new suppressor candidate on chromosome 13, in the BRCA2-Rb1 locus
OTHER SOURCE (OS): J. Steroid Biochem. Mol. Biol., 68 (1-2), 41-50 (1999)
CA 131:3561
REFERENCE:
AUTHOR (AU): Geck, P.; Szelei, J.; Jimenez, J.; Sonnenschein, C.; Soto, A.M.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (28-MAR-1997) Anatomy and Cell Biology,
Tufts
University Medical School, 136 Harrison Avenue,
Boston,
MA 02111, USA
REFERENCE:
AUTHOR (AU): Geck, P.; Szelei, J.; Jimenez, J.; Sonnenschein, C.; Soto, A.M.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (05-APR-1999) Anatomy and Cell Biology,
Tufts
University Medical School, 136 Harrison Avenue,
Boston,
MA 02111, USA
FEATURES (FEAT):

FEATURES (FEAT):

Feature Key	Location	Qualifier
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exons 2-24 map to cosmid 267p19;
exons 25-34 map to P1 Artificial
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L3 ANSWER 1 OF 1

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LOCUS (LOC): AC068224 GenBank (R)
GenBank ACC. NO. (GBN): **AC068224**
CAS REGISTRY NO. (RN): 263690-85-3
SEQUENCE LENGTH (SQL): 54398
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): High Throughput Genome Sequencing
DATE (DATE): 30 Apr 2000
DEFINITION (DEF): Homo sapiens chromosome 3 clone RP11-660H19 map 3,
LOW-PASS SEQUENCE SAMPLING.
KEYWORDS (ST): HTG; HTGS_PHASE0
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates;
Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 13631 a 10245 c 8645 g 14936 t 6941 others
COMMENT:
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10161
Center clone name: 660_H_19

* NOTE: This record contains 68 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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* 2355 2454: gap of 100 bp
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* 3285 3959: contig of 675 bp in length
* 3960 4059: gap of 100 bp
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* 4747 4846: gap of 100 bp
* 4847 5564: contig of 718 bp in length
* 5565 5664: gap of 100 bp
* 5665 6360: contig of 696 bp in length
* 6361 6460: gap of 100 bp

* 6461 7132: contig of 672 bp in length
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AUTHOR (AU): Birren, B.; Linton, L.; Nusbaum, C.; Lander, E.
 TITLE (TI): Homo sapiens chromosome 3, clone RP11-660H19
 JOURNAL (SO): Unpublished
 REFERENCE: 2 (bases 1 to 54398)
 AUTHOR (AU): Birren, B.; Linton, L.; Nusbaum, C.; Lander, E.;
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 Zainoun, J.; Zimmer, A.; Zody, M.
 TITLE (TI): Direct Submission
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 for Genome Research, 320 Charles Street, Cambridge, MA
 02141, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
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L2 ANSWER 1 OF 1

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Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 1690 a 931 c 1037 g 1519 t
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AUTHOR (AU): Ohara,O.; Suyama,M.; Nagase,T.; Ishikawa,K.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (26-MAY-1998) to the DDBJ/EMBL/GenBank
databases. Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu,
Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
Tel:+81-438-52-3913, Fax:+81-438-52-3914)
OTHER SOURCE (OS): CA 129:171313
REFERENCE:
AUTHOR (AU): Ishikawa,K.; Nagase,T.; Suyama,M.; Miyajima,N.;
Tanaka,A.; Kotani,H.; Nomura,N.; Ohara,O.
TITLE (TI): Prediction of the coding sequences of unidentified
human genes. X. The complete sequences of 100 new cDNA
clones from brain which can code for large proteins in
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JOURNAL (SO): DNA Res., 5 (3), 169-176 (1998)

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LOCUS (LOC): AB023196 GenBank (R)
GenBank ACC. NO. (GBN): **AB023196**
CAS REGISTRY NO. (RN): 222526-42-3
SEQUENCE LENGTH (SQL): 5110
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 16 Jun 1999
DEFINITION (DEF): Homo sapiens mRNA for KIAA0979 protein, partial cds.
SOURCE: Homo sapiens adult male brain cDNA to mRNA,
clone_lib:pBluescriptII SK plus clone:hj07056.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates;
Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 1714 a 919 c 1045 g 1432 t
REFERENCE:
AUTHOR (AU): Nagase,T.; Ishikawa,K.; Suyama,M.; Kikuno,R.;
Hirosawa,M.; Miyajima,N.; Tanaka,A.; Kotani,H.;
Nomura,N.; Ohara,O.
TITLE (TI): Prediction of the coding sequences of unidentified
human genes. XIII. The complete sequences of 100 new
cDNA clones from brain which code for large proteins
in
vitro
JOURNAL (SO): DNA Res., 6 (1), 63-70 (1999)
OTHER SOURCE (OS): CA 131:28520
REFERENCE:
AUTHOR (AU): Ohara,O.; Nagase,T.; Kikuno,R.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (04-FEB-1999) to the DDBJ/EMBL/GenBank
databases. Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu,
Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
Tel:+81-438-52-3913, Fax:+81-438-52-3914)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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gene	1..4253	/gene="KIAA0979"
CDS	<1..4253	/gene="KIAA0979" /codon-start=3 /product="KIAA0979 protein" /protein-id="BAA76823.1" /db-xref="GI:4589602" /translation="VRRLKMOVVKTFMDMDQDSEE EKELYLNLAHLASDFFLKHPDKD VRLLVACCLADIFRIYAPEAPYTPDKLKDFMF ITRQLKGLEDTKSPQFNRYFYLLE NIAWVKSÝNICFELEDSNEIFTQLYRTLFSVINN

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LOCUS (LOC): HSU50533 GenBank (R)
GenBank ACC. NO. (GBN): U50533
CAS REGISTRY NO. (RN): 180884-10-0
SEQUENCE LENGTH (SQL): 1852
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 27 Nov 1996
DEFINITION (DEF): Human BRCA2 region, mRNA sequence CG008.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates;
Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 609 a 348 c 379 g 505 t 11 others
REFERENCE:
AUTHOR (AU): Couch,F.J.; Rommens,J.M.; Neuhausen,S.L.; Belanger,C.;
Dumont,M.; Kenneth,A.; Bell,R.; Berry,S.; Bogden,R.;
Cannon-Albright,L.; Farid,L.; Frye,C.; Hattier,T.;
Janecki,T.; Jiang,P.; Kehrer,R.; Leblanc,J.-F.;
McArthur-Morrison,J.; McSweeney,D.; Miki,Y.; Peng,Y.;
Samson,C.; Schroeder,M.; Snyder,S.C.; Stringfellow,M.;
Stroup,C.; Swedlund,B.; Swensen,J.; Teng,D.;
Thakur,S.;
Tran,T.; Tranchant,M.; Welver-Feldhaus,J.;
Wong,A.K.C.;
Shizuya,H.; Labrie,F.; Skolnick,M.H.; Goldgar,D.E.;
Kamb,A.; Weber,B.L.; Tavtigian,S.V.; Simard,J.
TITLE (TI): Generation of an integrated transcription map of the
BRCA2 region on chromosome 13q12-q13
JOURNAL (SO): Genomics, 36 (1), 86-99 (1996)
OTHER SOURCE (OS): CA 125:187182
REFERENCE:
AUTHOR (AU): Simard,J.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (04-MAR-1996) Jacques Simard, Laboratory of
Molecular Endocrinology, CHUL Research Center, 2705,
Boulevard Laurier, Quebec City, Quebec G1V 4G2, Canada

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1852	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="13" /map="13q12-q13" /note="CG008; DSEG numbers: D13S171 and D13S310"

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421 tgtggaaatg tcaaaatctg ctccgacatc aagtaaagga tttgcttgac ttgattaagc
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